CLAIMS

What is claimed is:

1. A method of making a biosensor capable of detecting a molecule, wherein the molecules is a ligand being capable of binding an olfactory receptor protein, said method comprising the steps of:

(a) determining the amino acid sequence of a preselected olfactory receptor protein, the secondary and tertiary structures of said olfactory receptor protein being unknown;

(b) comparing the amino acid sequence of said preselected olfactory receptor protein to known amino acid sequences of transmembrane proteins having known, secondary and tertiary structures, said known amino acid sequence of said transmembrane proteins being selected from the group consisting of G-protein coupled receptors;

(c) selecting at least one of said known amino acid sequences of transmembrane proteins by determining which of said known amino acid sequences has the highest degree of sequence homology with the amino acid sequence of said preselected olfactory receptor protein;

(d) using said selected sequence to approximate the secondary and tertiary structure of said preselected olfactory receptor protein;

(e) using said approximated secondary and tertiary structures of said olfactory receptor protein to identify a likely binding domain of said olfactory receptor protein for said ligand;

(f) synthesizing a peptide having the primary structure of said likely binding domain; and

(g) attaching said synthesized peptide to the surface of a transducer.

2. A method of making a biosensor capable of detecting a gas molecule, the method comprising:

obtaining an amino acid sequence of an olfactory receptor protein ORP;

using the amino acid sequence of the ORP to compute a predictive secondary structure of the ORP and predict transmembrane fragments of the ORP;

comparing the amino acid sequence of the ORP with G-protein coupled receptors (GPCRs) by Basic Local Alignment Search Tool (BLAST) to find a template protein having the highest primary sequence homology with the ORP, wherein the primary, secondary and tertiary structures of the GPCRs are known and the secondary structures of the GPCRs are similar to the predictive secondary structure of the ORP;

using the tertiary structure of the template protein to be an initial tertiary structure for the ORP to compute a predictive tertiary structure of the ORP by energy minimization and molecular dynamics to get three coordinates of each ORP's atom;

treating the ORP as a rigid body, according to the three coordinates of each ORP's atom, to calculate geometrical binding domains of the ORP with a gas molecule by geometric recognition algorithms;

relaxing the ORP's structure to further calculating the most probably binding domains, based on the geometrical binding domains, of the ORP with the gas molecule;

synthesizing peptides according to the primary amino acid sequence of the likely binding domains; and

attaching the synthesized peptide to a surface of a transducer having a gold electrode on a piezoelectric quartz to be a receptor of a biosensor.

3. The method of claim 2, wherein a molecule containing thiol functional group is added to a terminal of the synthesized peptides when two terminals of the synthesized peptides do not have thiol functional group.

4. The method of claim 3, wherein attaching the synthesized peptide to the surface of the transducer comprises:

dissolving the synthesized peptides in a solvent to form a peptide solution; and

dipping the gold electrode in the peptide solution under room temperature.

5. A method of finding candidates for peptides being covered on an electronic nose for detecting a gas, the method comprising:

obtaining an amino acid sequence of an olfactory receptor protein ORP;

using the amino acid sequence of the ORP to compute a predictive secondary structure of the ORP and predict transmembrane fragments of the ORP;

comparing the amino acid sequence of the ORP with G-protein coupled receptors (GPCRs) by Basic Local Alignment Search Tool (BLAST) to find a template protein having the highest primary sequence homology with the ORP, wherein the primary, secondary and tertiary structures of the GPCRs are known and the secondary structures of the GPCRs are similar to the predictive secondary structure

of the ORP;

using the tertiary structure of the template protein to be an initial tertiary structure for the ORP to compute a predictive tertiary structure of the ORP by energy minimization and molecular dynamics to get three coordinates of each ORP's atom;

treating the ORP as a rigid body, according to the three coordinates of each ORP's atom, to calculate geometrical binding domains of the ORP with a gas molecule by geometric recognition algorithms; and

relaxing the ORP's structure to further calculating the most probably binding domains, based on the geometrical binding domains, of the ORP with the gas molecule, whereby amino acid sequences of the most probably binding domains are candidates for peptides being covered on an electronic nose.